

REPEAT-FREE PROBES FOR MOLECULAR CYTOGENETICS

ABSTRACT OF THE DISCLOSURE

The present invention provides a rapid, efficient, and automated method for identifying unique sequences within the genome. This invention involves the identification of repeat sequence-free subregions within a genomic region of interest as well as the determination of which of those repeat sequence-free subregions are truly unique within the genome. Once the truly unique subregions are identified, primer sequences are generated that are suitable for the amplification of sequences, *e.g.*, for use as probes or array targets, within the unique subregions.

SF 1179940 v1